Amendments to the Specification:

Sequence Listing

On August 16, 2002, Applicants submitted a Sequence Listing in response to a Notice of Defective Response. Applicants respectfully request the specification be amended to include the paper copy of the Sequence Listing submitted on August 16, 2002. Please insert the sequence listing after the Abstract.

10/11/07

Please replace the paragraph beginning at page 37, lines 10-~~16~~ 24, with the following rewritten paragraph:

The full-length native sequence TCCR genes encoding the polypeptides described in Figure 3 (SEQ ID NO: 1) and Figure 4 (SEQ ID NO:2), or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length TCCR cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of TCCR or TCCR from other species) which have a desired sequence identity to the TCCR polynucleotide sequence encoding the polypeptides disclosed in Figures 3 and 4 (SEQ ID NO:s 1&2, respectively). Optionally, the length of the probes will be about 20 to 50 bases. The hybridization probes may be derived from regions of the nucleotide sequence encoding the polypeptides of SEQ ID NO: 1&2 wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence TCCR. By way of example, a screening method will comprise isolating the coding region of the TCCR gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TCCR gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine to which members of such libraries the probe hybridizes. Hybridization techniques are described in further detail in the Examples below. Any EST or other sequence fragments disclosed herein may similarly be employed as probes, using the methods disclosed herein.